

SEQUENCE LISTING

(1) GENERAL INFORMATION:

- (i) APPLICANT: Hillman, Jennifer L.  
Corley, Neil C.  
Baughn, Mariah R.
- (ii) TITLE OF INVENTION: DELTA 1-PYRROLINE-5-CARBOXYLATE REDUCTASE  
HOMOLOG
- (iii) NUMBER OF SEQUENCES: 3
- (iv) CORRESPONDENCE ADDRESS:  
(A) ADDRESSEE: Incyte Pharmaceuticals, Inc.  
(B) STREET: 3174 Porter Drive  
(C) CITY: Palo Alto  
(D) STATE: CA  
(E) COUNTRY: USA  
(F) ZIP: 94304
- (v) COMPUTER READABLE FORM:  
(A) MEDIUM TYPE: Diskette  
(B) COMPUTER: IBM Compatible  
(C) OPERATING SYSTEM: Windows  
(D) SOFTWARE: FastSEQ for Windows Version 2.0b
- (vi) CURRENT APPLICATION DATA:  
(A) APPLICATION NUMBER: TO BE ASSIGNED  
(B) FILING DATE: HERewith  
(C) CLASSIFICATION:
- (vii) PRIOR APPLICATION DATA:  
(A) APPLICATION NUMBER:  
(B) FILING DATE:
- (viii) ATTORNEY/AGENT INFORMATION:  
(A) NAME: Cerrone, Michael C  
(B) REGISTRATION NUMBER: 39,132  
(C) REFERENCE/DOCKET NUMBER: PF-0532 US
- (ix) TELECOMMUNICATION INFORMATION:  
(A) TELEPHONE: 650-855-0555  
(B) TELEFAX: 650-855-0572  
(C) TELEX:

(2) INFORMATION FOR SEQ ID NO:1:

- (i) SEQUENCE CHARACTERISTICS:  
(A) LENGTH: 314 amino acids  
(B) TYPE: amino acid  
(C) STRANDEDNESS: single  
(D) TOPOLOGY: linear
- (vii) IMMEDIATE SOURCE:  
(A) LIBRARY: PROSNON01

(B) CLONE: 2278458

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

Met	Ser	Val	Gly	Phe	Ile	Gly	Ala	Gly	Gln	Leu	Ala	Tyr	Arg	Phe	Thr
1				5					10					15	
Ala	Ala	Gly	Ile	Leu	Ser	Ala	His	Lys	Ile	Ile	Ala	Ser	Ser	Pro	Glu
			20					25					30		
Met	Asn	Leu	Pro	Thr	Val	Ser	Ala	Leu	Arg	Lys	Met	Gly	Val	Asn	Leu
	35						40					45			
Thr	Arg	Ser	Asn	Lys	Glu	Thr	Val	Lys	His	Ser	Asp	Val	Leu	Phe	Leu
	50					55					60				
Ala	Val	Lys	Pro	His	Ile	Ile	Pro	Phe	Ile	Leu	Asp	Glu	Ile	Gly	Ala
65					70					75				80	
Asp	Val	Gln	Ala	Arg	His	Ile	Val	Val	Ser	Cys	Ala	Ala	Gly	Val	Thr
				85					90					95	
Ile	Ser	Ser	Val	Glu	Lys	Lys	Leu	Met	Ala	Phe	Gln	Pro	Ala	Pro	Lys
			100					105					110		
Val	Ile	Arg	Cys	Met	Thr	Asn	Thr	Pro	Val	Val	Val	Gln	Glu	Gly	Ala
		115					120						125		
Thr	Val	Tyr	Ala	Thr	Gly	Thr	His	Ala	Leu	Val	Glu	Asp	Gly	Gln	Leu
	130					135					140				
Leu	Glu	Gln	Leu	Met	Ser	Val	Gly	Phe	Cys	Thr	Glu	Val	Glu	Glu	
145					150				155					160	
Asp	Leu	Ile	Asp	Ala	Val	Thr	Gly	Leu	Ser	Gly	Ser	Gly	Pro	Ala	Tyr
				165					170					175	
Ala	Phe	Met	Ala	Leu	Asp	Ala	Asp	Gly	Gly	Val	Lys	Met	Gly	Leu	Pro
			180					185					190		
Arg	Arg	Leu	Ala	Ile	Gln	Leu	Gly	Ala	Gln	Ala	Leu	Leu	Gly	Ala	Ala
		195					200						205		
Lys	Met	Leu	Leu	Asp	Ser	Glu	Gln	His	Pro	Cys	Gln	Leu	Lys	Asp	Asn
	210					215					220				
Val	Cys	Ser	Pro	Gly	Gly	Ala	Thr	Ile	His	Ala	Leu	His	Phe	Leu	Glu
225					230					235					240
Ser	Gly	Gly	Phe	Arg	Ser	Leu	Leu	Ile	Asn	Ala	Val	Glu	Ala	Ser	Cys
				245					250					255	
Ile	Arg	Thr	Arg	Glu	Leu	Gln	Ser	Met	Ala	Asp	Gln	Glu	Lys	Ile	Ser
			260					265					270		
Pro	Ala	Ala	Leu	Lys	Lys	Thr	Leu	Leu	Asp	Arg	Val	Lys	Leu	Glu	Ser
		275					280						285		
Pro	Thr	Val	Ser	Thr	Leu	Thr	Pro	Ser	Ser	Pro	Gly	Lys	Leu	Leu	Thr
	290					295					300				
Arg	Ser	Leu	Ala	Leu	Gly	Gly	Lys	Lys	Asp						
305						310									

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1742 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(vii) IMMEDIATE SOURCE:

- (A) LIBRARY: PROSNON01
- (B) CLONE: 2278458

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

GCGCCATCAG	CCGCCCGGGA	GATATCCGCC	GGGGGAGAAT	AGGGTTGCAC	CATCCCAGAA	60
GCTGCTGTTA	GCTCGCCGGT	CCTCGGCACG	CCGCCCGTTC	GCCCCTGCGC	TGTCCGCCCT	120

TCCCTAGCG	TTACTTCCGG	TCCCTCGCTG	AGGGGGTTCG	TGCGGCTCCC	AGGAGGCGTG	180
AACCGCGGAC	CATGAGCGTG	GGCTTCATCG	GGGCCGGCCA	GCTGGCCTAT	GCTCTGGCGC	240
GGGGCTTCAC	GGCCGCAGGC	ATCCTGTCGG	CTCACAAGAT	AATAGCCAGC	TCCCCAGAAA	300
TGAACCTGCC	CACGGTGTC	GCGCTCAGGA	AGATGGGTGT	GAACCTGACA	CGCAGCAACA	360
AGGAGACGGT	GAAGCACAGC	GACGTCCGTG	TTCTGGCTGT	GAAGCCACAT	ATCATCCCCT	420
TCATCCTGGA	TGAGATTGGG	GCCGACGTGC	AAGCCAGACA	CATCGTGGTC	TCCTGTGCGG	480
CTGGTGTAC	CATCAGCTCT	GTGGAGAAGA	AGCTGATGGC	ATTCCAGCCA	GCCCCAAAG	540
TGATTTCGTG	CATGACCAAC	ACACCTGTGG	TAGTGCAGGA	AGGCGCTACA	GTGTACGCCA	600
CGGGCACCCA	TGCCCTGGTG	GAGGATGGGC	AGCTCCTGGA	GCAGCTCATG	AGCAGCGTGG	660
GCTTCTGCAC	TGAGGTGGAA	GAGGACCTCA	TCGATGCCGT	CACGGGGCTC	AGTGGCAGCG	720
GGCCTGCCTA	TGCATTTCATG	GCTCTGGACG	CATTGGCTGA	TGGTGGGGTG	AAGATGGGTT	780
TGCCACGGCG	CCTGGCAATC	CAACTCGGGG	CCCAGGCTTT	GCTGGGAGCT	GCCAAGATGC	840
TGCTGGACTC	GGAGCAGCAT	CCATGCCAGC	TTAAGGACAA	TGTCTGCTCC	CCTGGGGGAG	900
CCACCATCCA	CGCCCTGCAC	TTTCTAGAGA	GTGGGGGCTT	CCGCTCTCTG	CTCATCAATG	960
CAGTTGAGGC	CTCCTGTATC	CGAACACGAG	AGCTACAGTC	CATGGCCGAC	CAAGAAAAGA	1020
TCTCCCCAGC	TGCCCTTAAG	AAGACCCTCT	TAGACAGAGT	GAAGCTGGAA	TCCCCACAG	1080
TCTCCACACT	GACCCCTTCC	AGCCCAGGGA	AGCTCCTCAC	AAGAAGCCTG	GCCCTGGGAG	1140
GCAAGAAGGA	CTAAGGCAGC	ATCTGTCCCC	TCTGTGATTG	AGAGCCCTTA	GTTGAGAGCC	1200
CCTGCCGGCC	CTGCCACCCC	CCTGCCCCGC	TCCCACCATT	GCCCCCTCTC	AGCTGTGCAA	1260
GGAGAAAGCA	TGCTTAGGAA	GTTTTAGGT	CCTTGTGATA	AAACCTCCTT	AAATCTGTTC	1320
AGACCAAGCA	ATGCGAGCTT	CCTCTCCTGT	CCCATGTTGG	AAGTTGCTCT	GAAGGGGTGG	1380
TAGATGCTGG	AAGCCAGACA	CAACCCTGCG	TACGCTGCTC	AGTTGGTGGA	GAAGGGGGCT	1440
GGGACTGGAG	TCAGCCCAGC	TGGGAGGAGG	GGCTGGGGAG	GATCTGCAGC	TGAAGCCCGA	1500
GGCAGGGTTG	GTGTGATGCC	AAGGCAAAGT	GGTGAGGAGA	AAACAGGAAA	CGGGCTTTCT	1560
CTGAATTGGT	AAATGGGAAA	GAAGTGAGCA	ACTTAAGATT	ATCACAATTA	ATCACAAGTG	1620
TACAGGATTA	GACTGGGTTT	ATATTTAACT	CTTGCTTCAT	AGGTGTACCA	TTTAAAGAGT	1680
GTTATTTAAT	GCTAAGTTTA	ACTGCTTTAA	TAAAGTTTAT	TTTTAAATAT	CAAAAAAAAA	1740
AA						1742

## (2) INFORMATION FOR SEQ ID NO:3:

## (i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 315 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

## (vii) IMMEDIATE SOURCE:

- (A) LIBRARY: GENBANK
- (B) CLONE: 189498

## (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

Met	Ser	Val	Gly	Phe	Ile	Gly	Ala	Gly	Gln	Leu	Ala	Phe	Ala	Lys	Gly
1				5				10						15	
Phe	Thr	Ala	Ala	Gly	Val	Leu	Ala	Ala	His	Lys	Ile	Met	Ala	Ser	Ser
			20					25					30		
Pro	Asp	Met	Asp	Leu	Ala	Thr	Val	Ser	Ala	Leu	Arg	Lys	Met	Gly	Val
			35					40					45		
Lys	Leu	Thr	Pro	His	Asn	Lys	Glu	Thr	Val	Gln	His	Ser	Asp	Val	Leu
			50				55					60			
Phe	Leu	Ala	Val	Lys	Pro	His	Ile	Ile	Pro	Phe	Ile	Leu	Asp	Glu	Ile
65						70				75				80	
Gly	Ala	Asp	Ile	Glu	Asp	Arg	His	Ile	Val	Val	Ser	Cys	Ala	Ala	Gly
				85					90					95	
Val	Thr	Ile	Ser	Ser	Ile	Glu	Lys	Lys	Leu	Ser	Ala	Phe	Arg	Pro	Ala
			100					105					110		
Pro	Arg	Val	Ile	Arg	Cys	Met	Thr	Asn	Thr	Pro	Val	Val	Val	Arg	Glu
			115				120						125		
Gly	Ala	Thr	Val	Tyr	Ala	Thr	Gly	Thr	His	Ala	Gln	Val	Glu	Asp	Gly
			130				135						140		

[illegible]

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